

IN THE SPECIFICATION

Please replace the paragraph immediately following the title with the following amended paragraph.

This application is the National Stage of International Application No. PCT/US99/24511, filed on October 19, 1999, which claims benefit under 35 U.S.C. § 119(e) of provisional application 60/172,221, filed on October 20, 1998, provisional application 60/118,559, filed on February 4, 1999, provisional application 60/172,229, filed on February 11, 1999, and provisional application 60/154,336, filed on April 22, 1999, all of which applications are hereby incorporated herein by reference.

Please replace the paragraph beginning at page 15, line 9 with the following amended paragraph:

Alternatively, a suite of commonly used and freely available sequence comparison algorithms is provided by the National Center for Biotechnology Information (NCBI) Basic Local Alignment Search Tool (BLAST) (Altschul, S.F. et al. (1990) J. Mol. Biol. 215:403-410), which is available from several sources, including the NCBI, Bethesda, MD, and on the Internet at <http://www.ncbi.nlm.nih.gov/BLAST/>. The BLAST software suite includes various sequence analysis programs including “blastn,” that is used to align a known polynucleotide sequence with other polynucleotide sequences from a variety of databases. Also available is a tool called “BLAST 2 Sequences” that is used for direct pairwise comparison of two nucleotide sequences. “BLAST 2 Sequences” can be accessed and used interactively at <http://www.ncbi.nlm.nih.gov/gorf/bl2.html>. The “BLAST 2 Sequences” tool can be used for both blastn and blastp (discussed below). BLAST programs are commonly used with gap and other parameters set to default settings. For example, to compare two nucleotide sequences, one may use blastn with the “BLAST 2 Sequences” tool Version 2.0.9 (May-07-1999) set at default parameters. Such default parameters may be, for example: